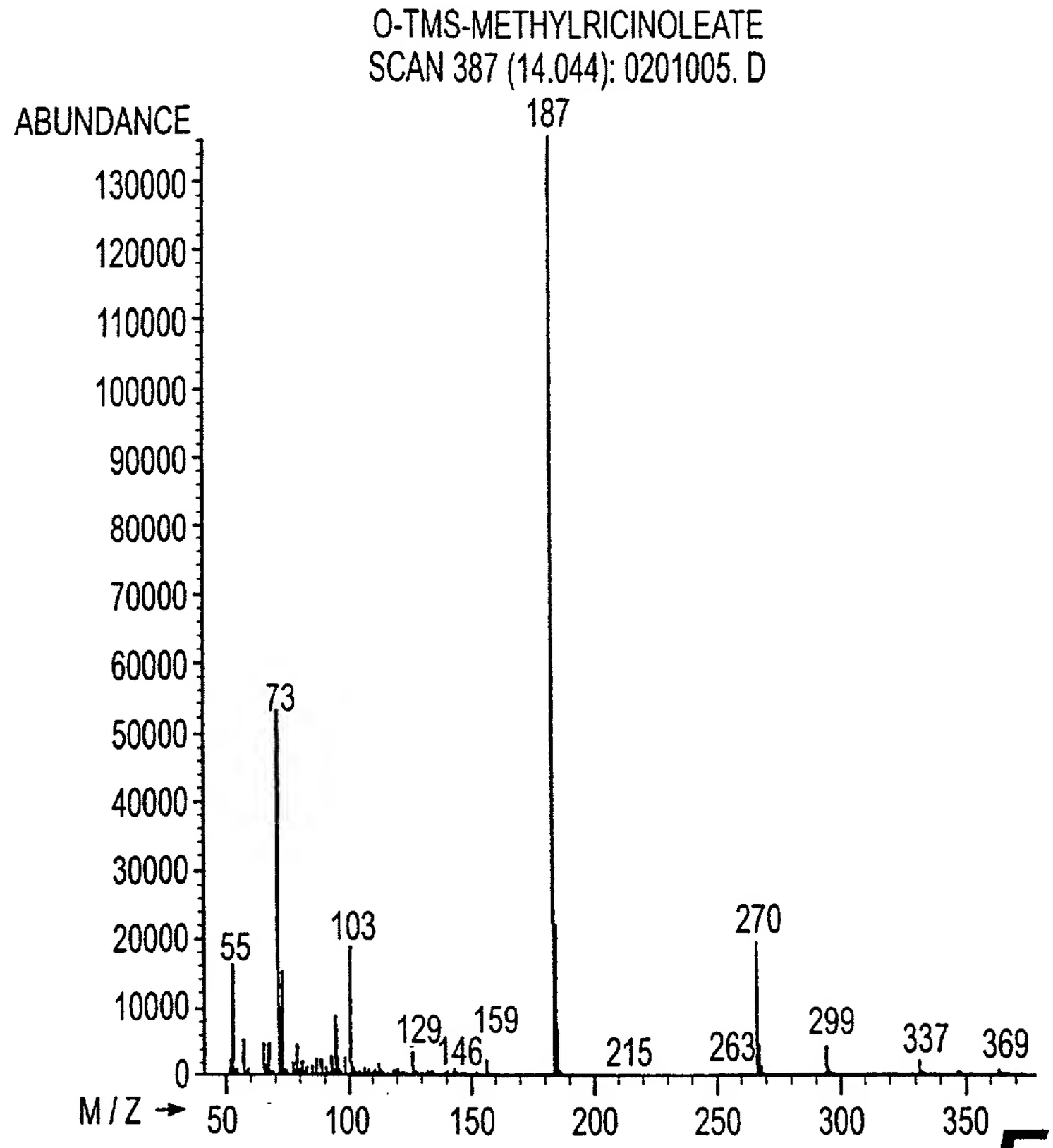

O-TMS-METHYLRICINOLEATE
SCAN 387 (14.044): 0201005. D
187
ABUNDANCE
130000
120000
110000
100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
73
55
103
129
146
159
215
263
270
299
337
369
M / Z →
50
100
150
200
250
300
350

FIG. 1A

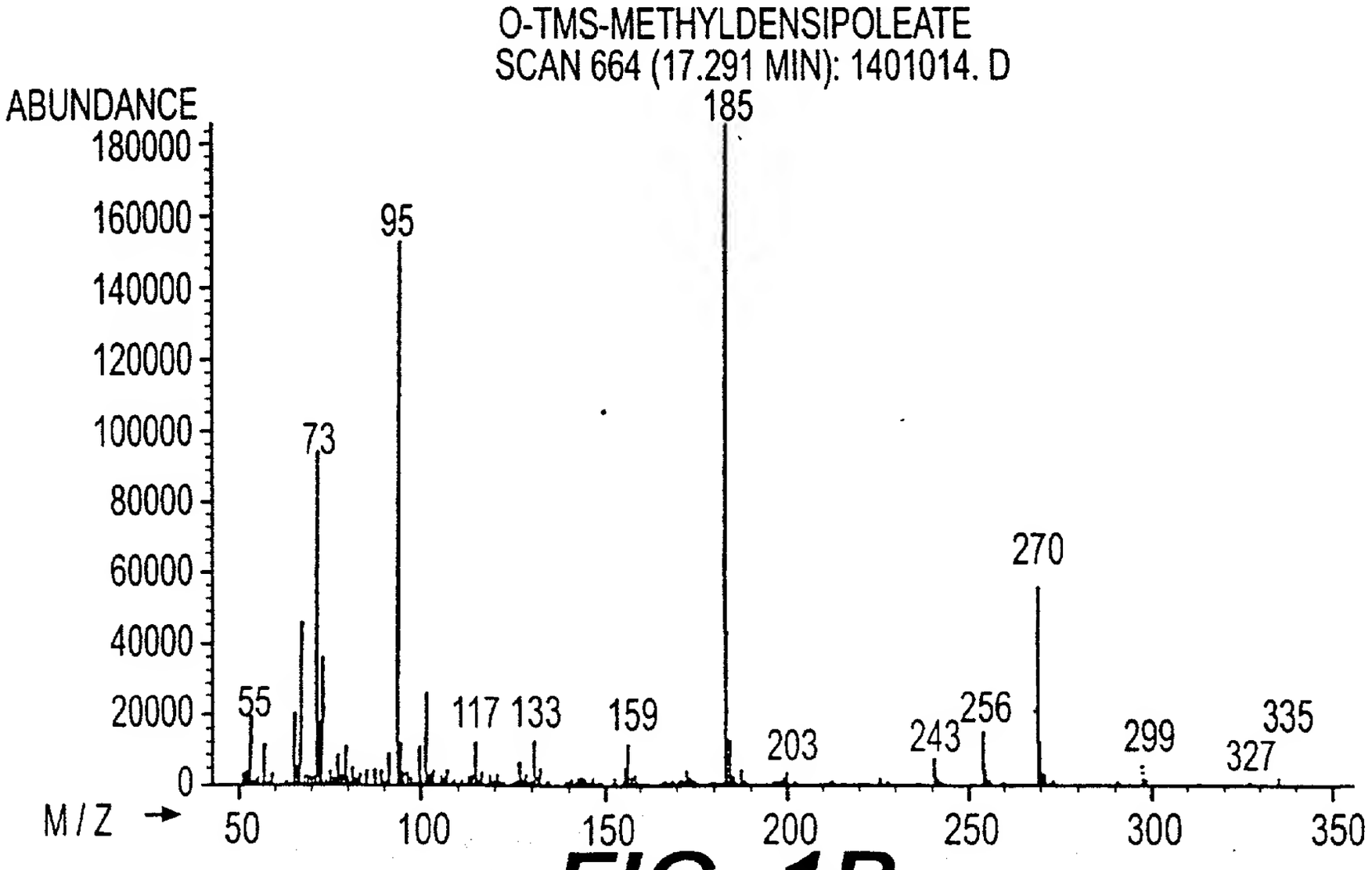

O-TMS-METHYLDENSIPOLEATE
SCAN 664 (17.291 MIN): 1401014. D
185
ABUNDANCE
180000
160000
140000
120000
100000
80000
60000
40000
20000
0
95
73
55
117
133
159
203
243
256
270
299
327
335
M / Z →
50
100
150
200
250
300
350

FIG. 1B

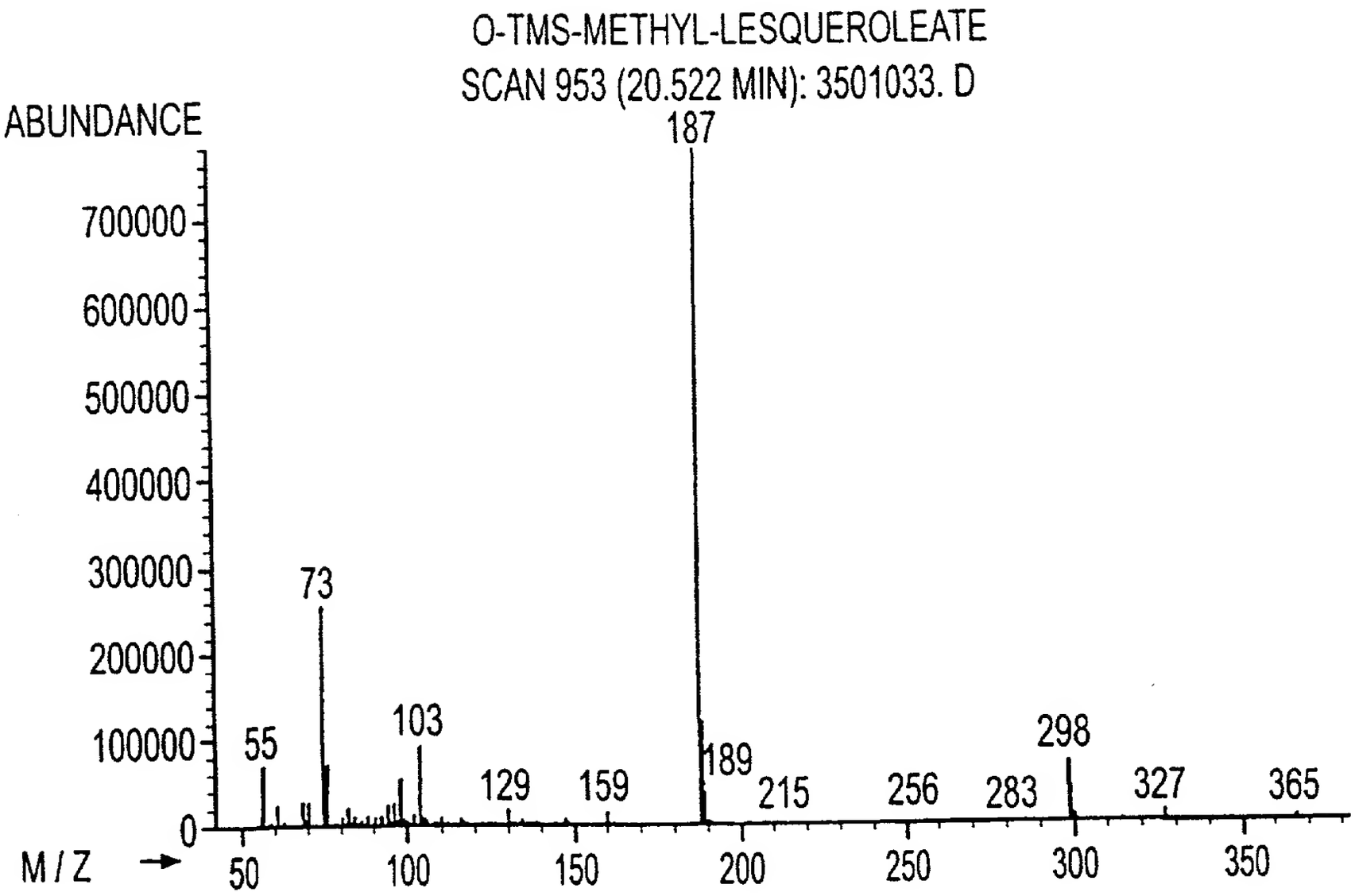

O-TMS-METHYL-LESQUEROLEATE
SCAN 953 (20.522 MIN): 3501033. D
ABUNDANCE
700000
600000
500000
400000
300000
200000
100000
0
M / Z
50
100
150
200
250
300
350
187
73
55
103
129
159
189
215
256
283
298
327
365

FIG. 1C

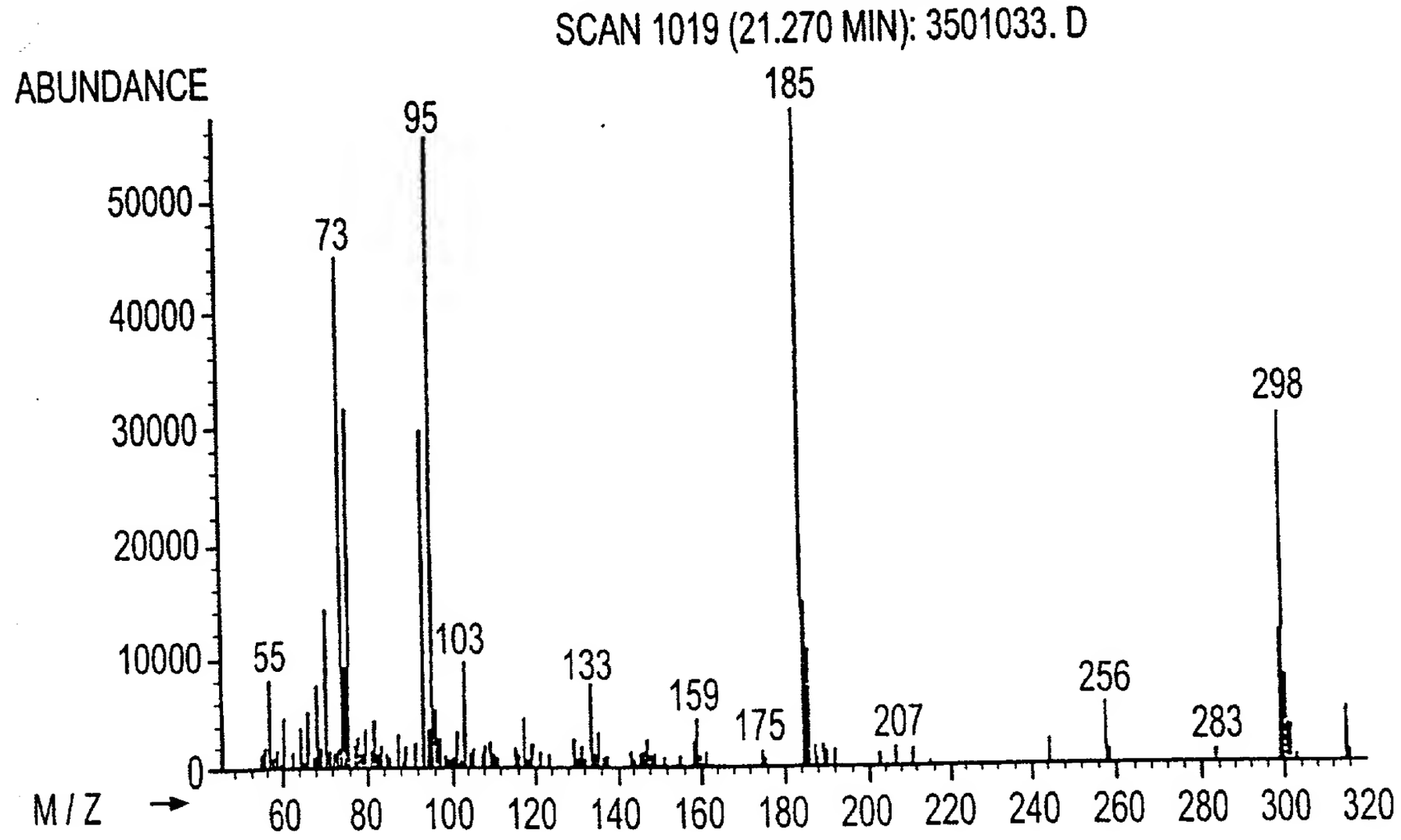
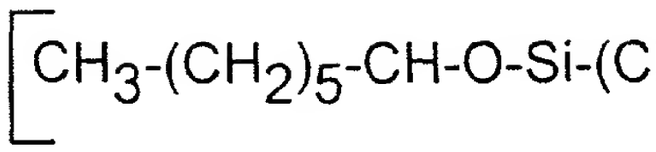
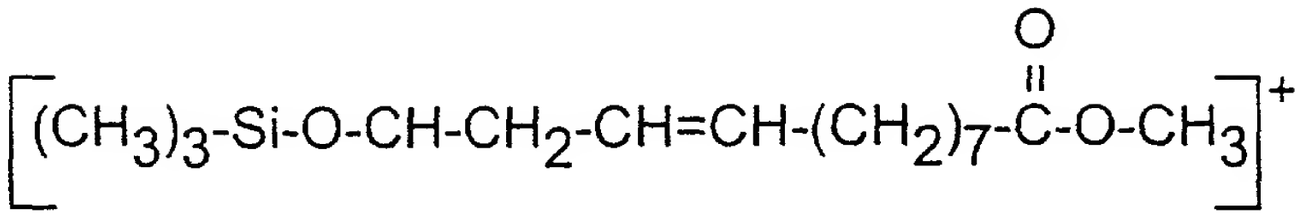

O-TMS-METHYLAURICOLEATE
SCAN 1019 (21.270 MIN): 3501033. D
ABUNDANCE
50000
40000
30000
20000
10000
0
M / Z
60
80
100
120
140
160
180
200
220
240
260
280
300
320
185
95
73
55
103
133
159
175
207
256
283
298

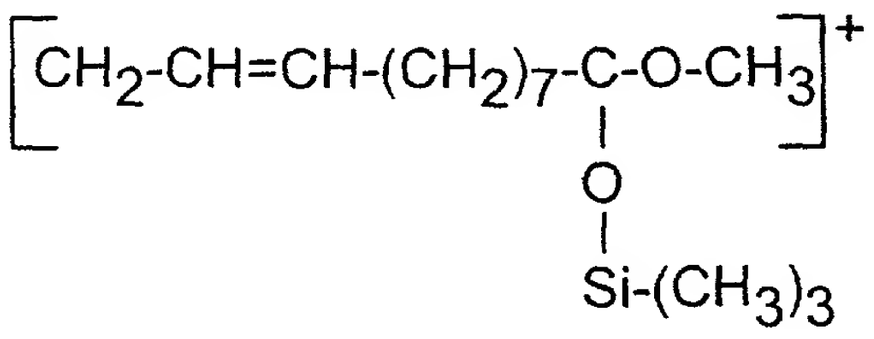
FIG. 1D

LON #1: MASS 187 

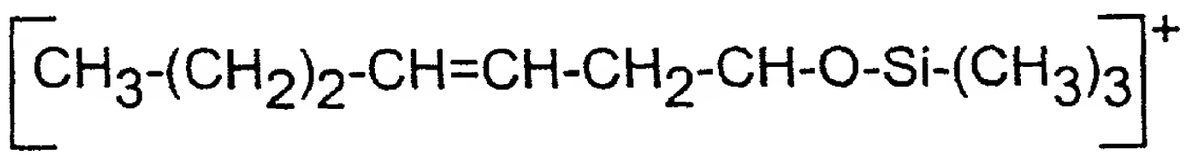
LON #2: MASS 299



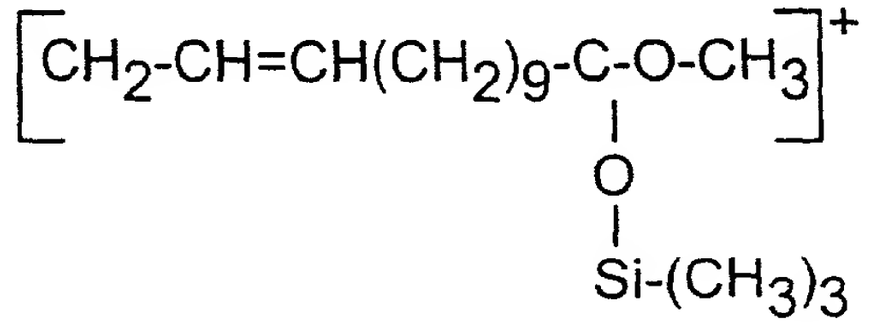
LON #3: MASS 270 (CHARACTERISTIC REARRANGEMENT ION)



LON #4: MASS 185 (DESATURATED ANALOG OF LON #1)



LON #5: MASS 298 (ELONGATED ANALOG OF LON #3)



LON #6: MASS 327 (ELONGATED ANALOG OF ION)

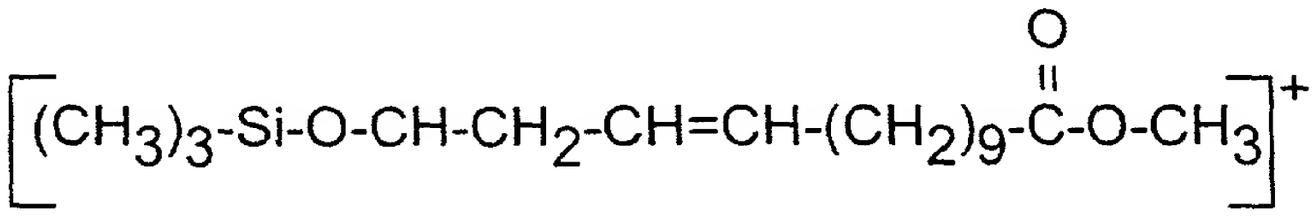


FIG. 2

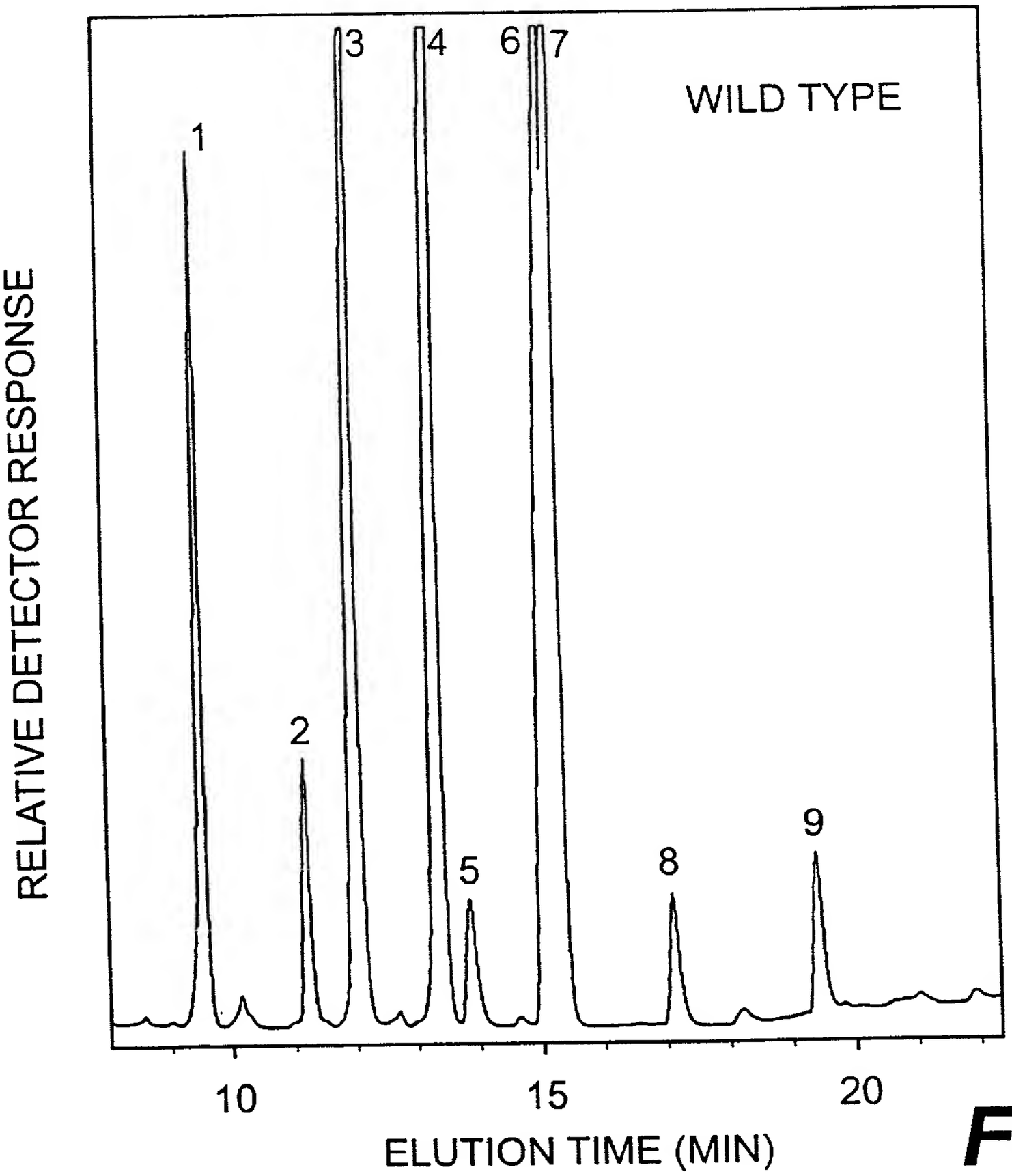

WILD TYPE
1
2
3
4
5
6
7
8
9
RELATIVE DETECTOR RESPONSE
10
15
20
ELUTION TIME (MIN)

FIG. 3A

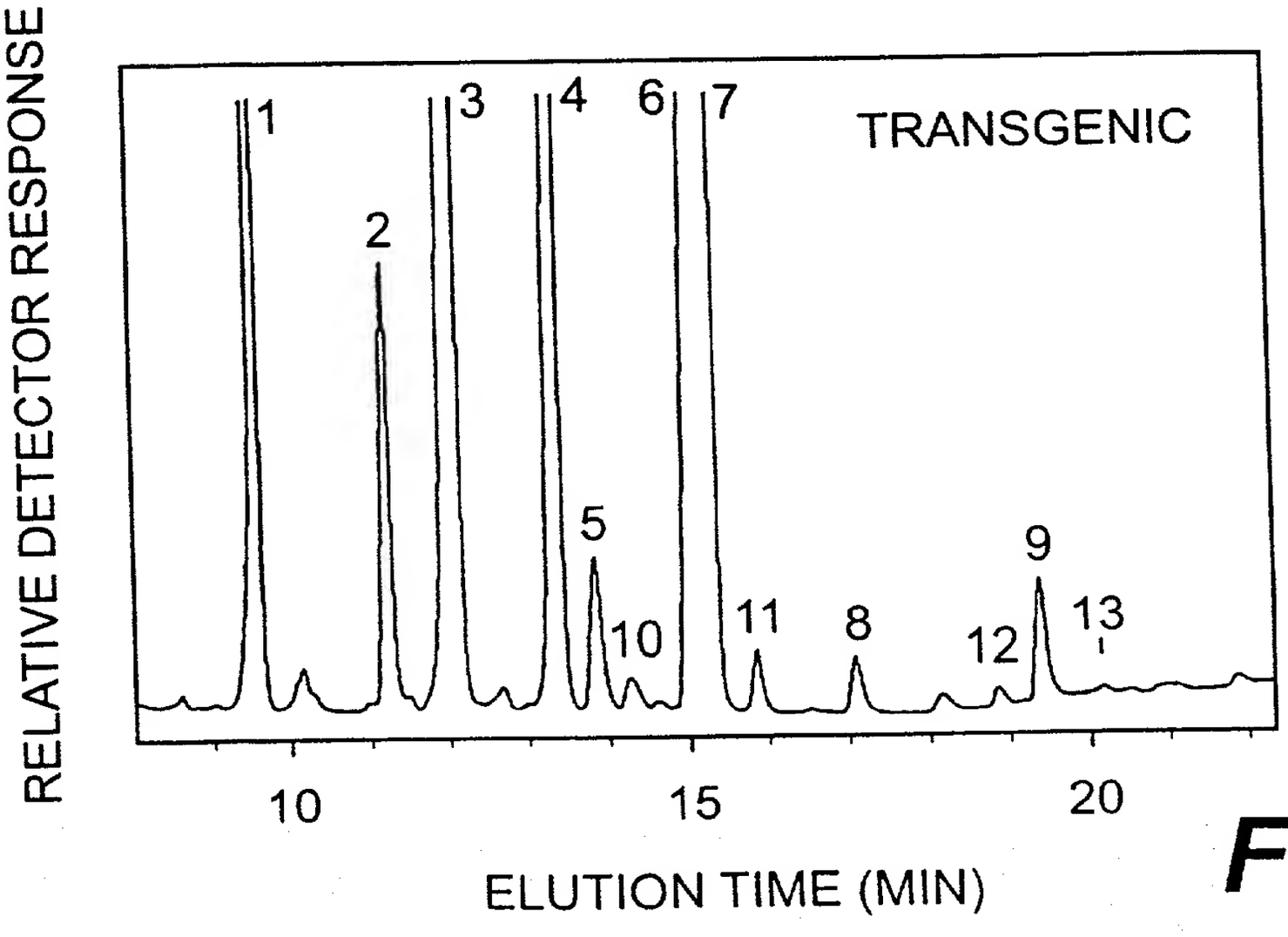

TRANSGENIC
1
2
3
4
5
6
7
8
9
10
11
12
13
RELATIVE DETECTOR RESPONSE
10
15
20
ELUTION TIME (MIN)

FIG. 3B

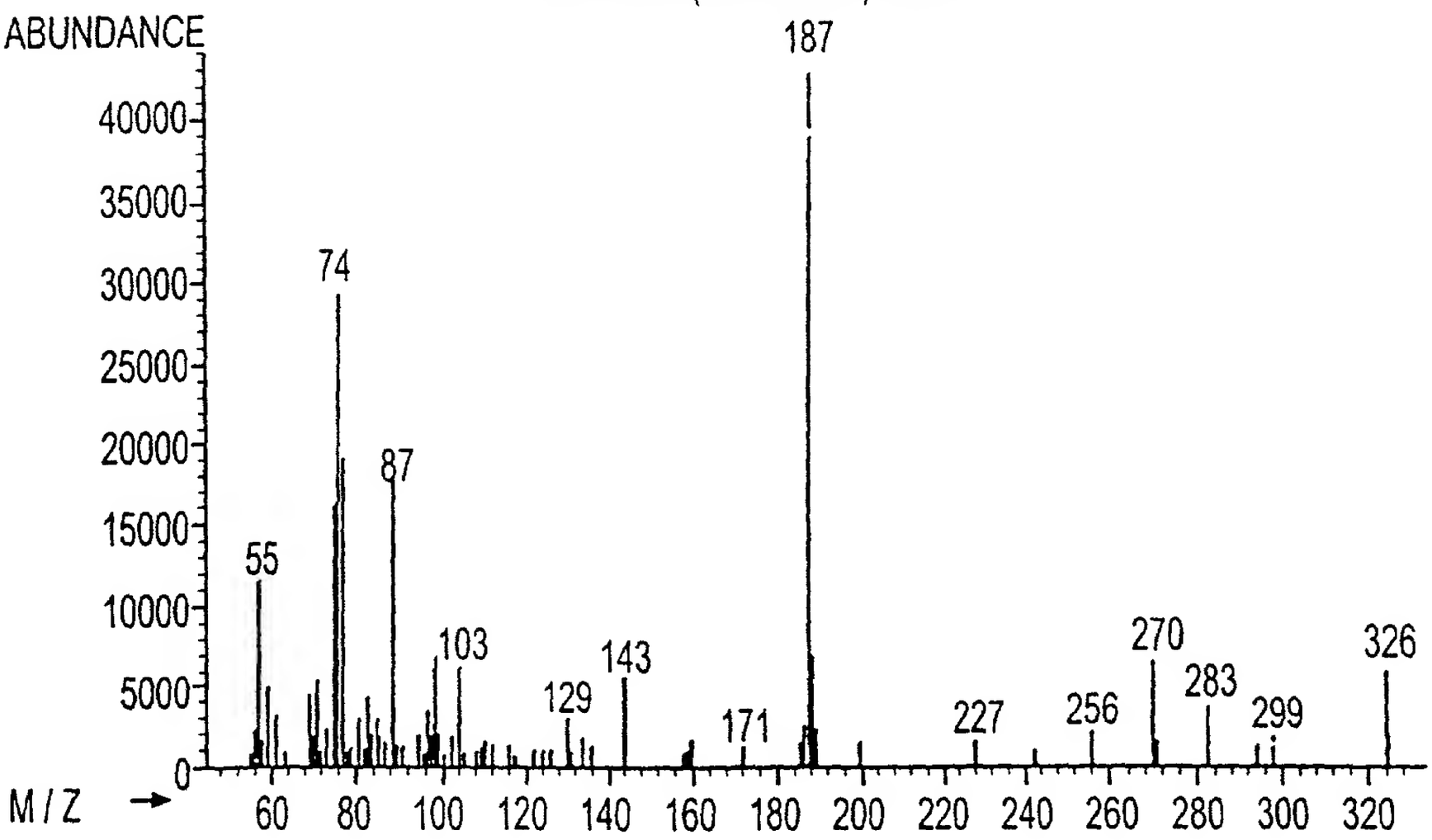

MASS SPECTRUM OF PEAK 10 FROM FIGURE 3B
SCAN 485 (15.203 MIN): 1501001. D
ABUNDANCE
M / Z
187
74
87
55
103
129
143
171
227
256
270
283
299
326
40000
35000
30000
25000
20000
15000
10000
5000
0
60
80
100
120
140
160
180
200
220
240
260
280
300
320

FIG. 4A

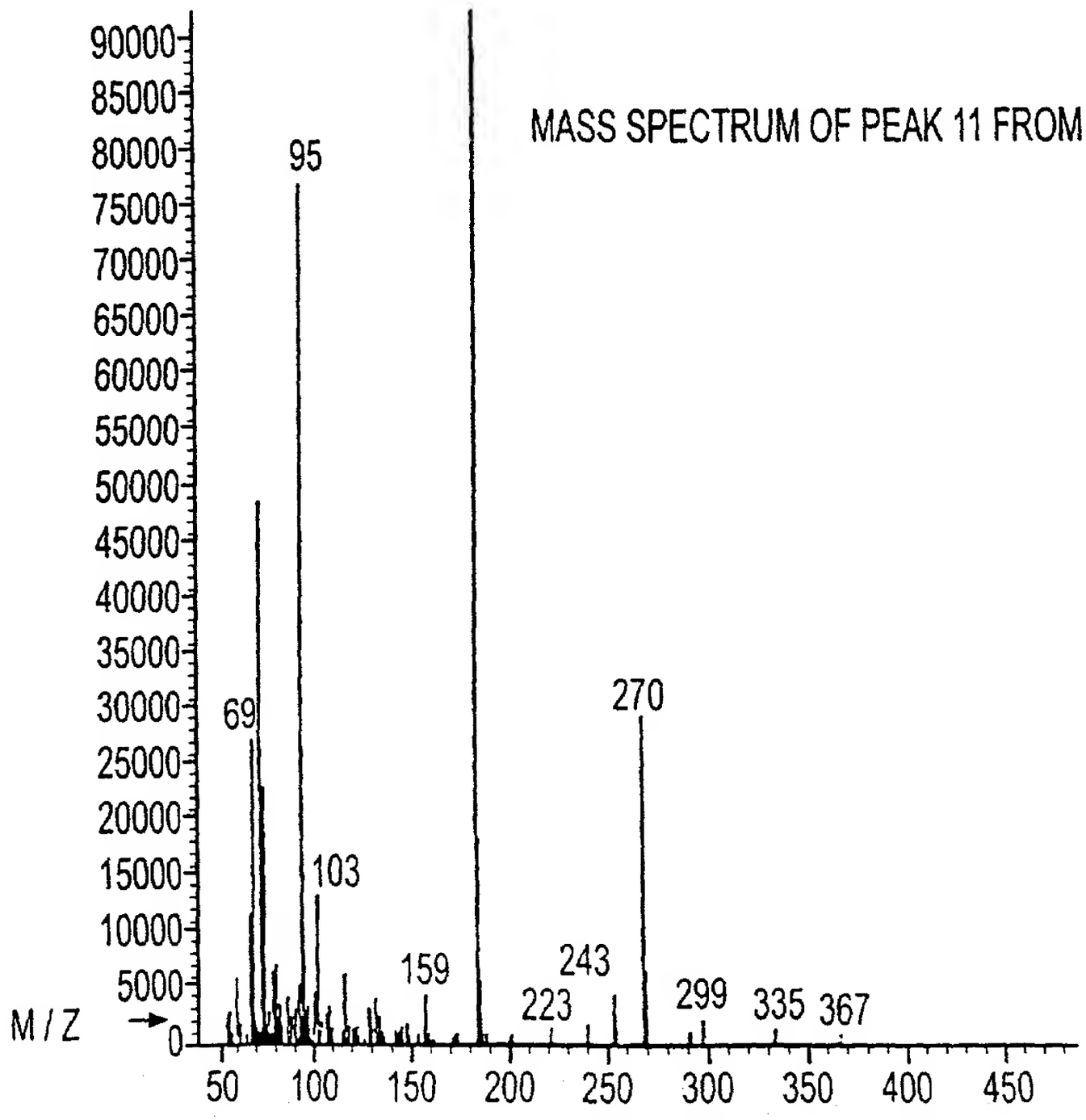

MASS SPECTRUM OF PEAK 11 FROM FIGURE 3B
M / Z
95
69
103
159
223
243
270
299
335
367
90000
85000
80000
75000
70000
65000
60000
55000
50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
50
100
150
200
250
300
350
400
450

FIG. 4B

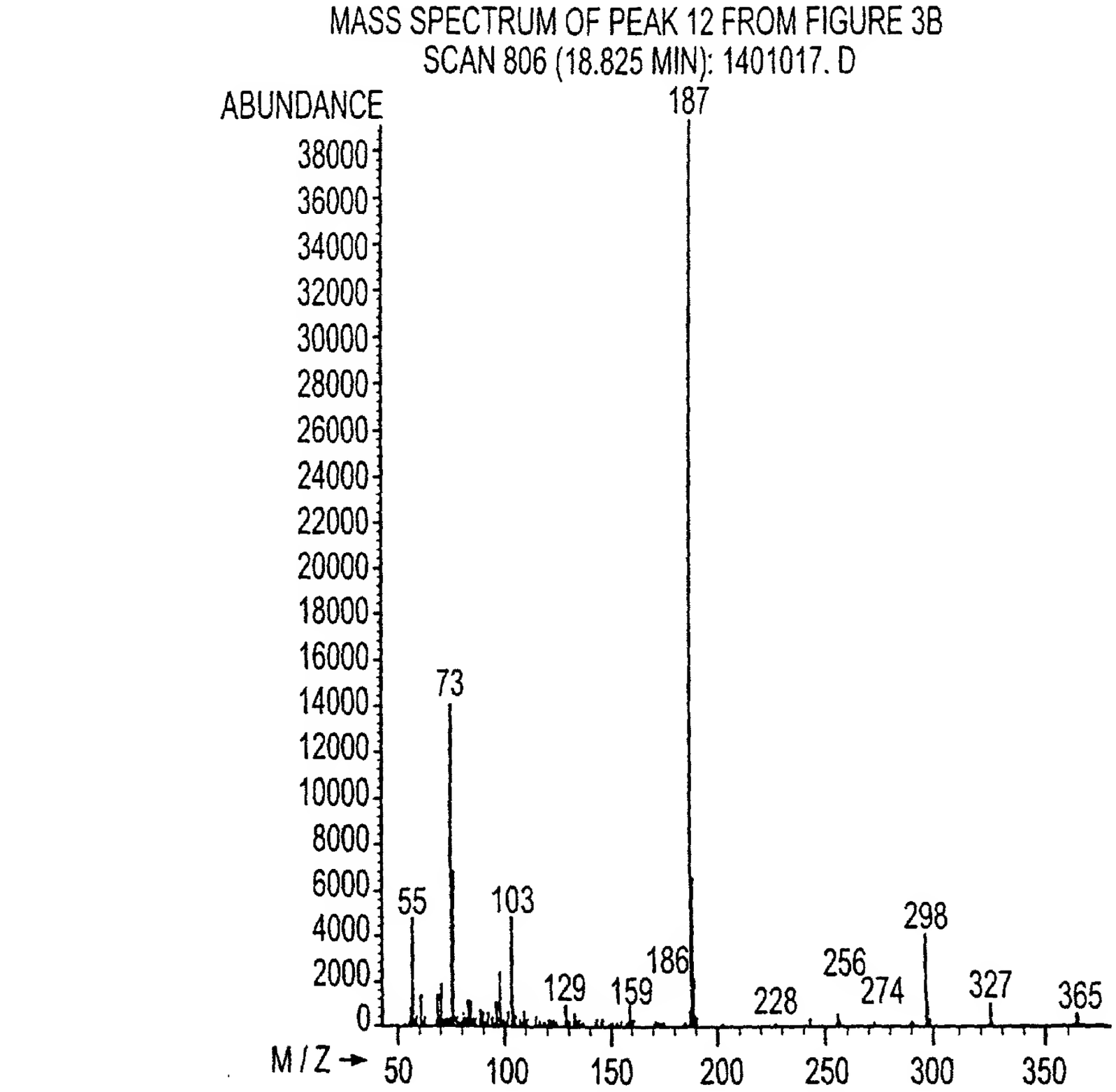

MASS SPECTRUM OF PEAK 12 FROM FIGURE 3B
SCAN 806 (18.825 MIN): 1401017. D
ABUNDANCE
38000
36000
34000
32000
30000
28000
26000
24000
22000
20000
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
M / Z →
50
100
150
200
250
300
350
73
187
55
103
129
159
186
228
256
274
298
327
365

FIG. 4C

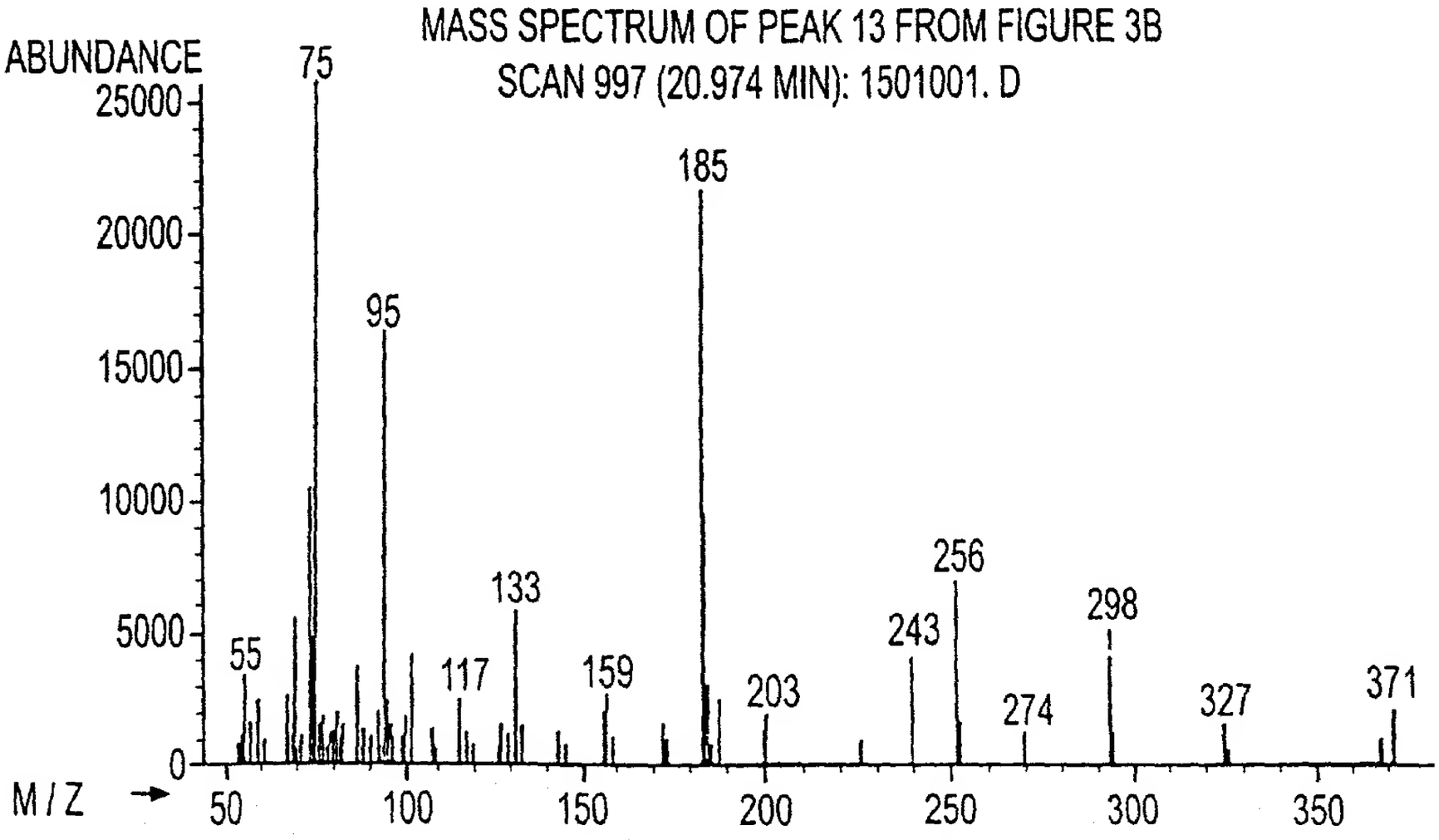

MASS SPECTRUM OF PEAK 13 FROM FIGURE 3B
SCAN 997 (20.974 MIN): 1501001. D
ABUNDANCE
25000
20000
15000
10000
5000
0
M / Z →
50
100
150
200
250
300
350
75
185
95
55
117
133
159
203
243
256
274
298
327
371

FIG. 4D

10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CATTTCTTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTTT	CCTTGTCTTG	GTCACTTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					
CAC					

FIG. 5

```
        10         20         30         40         50         60
TATAGGCACC GGAGGCACCA TTCCAACACA GGATCCCTCG AAAGAGATGA AGTATTTGTC
        70         80         90        100        110        120
CCAAAGCAGA AATCCGCAAT CAAGTGGTAC GGCGAATACC TCAACAACCC TCCTGGTCGC
       130        140        150        160        170        180
ATCATGATGT TAACTGTCCA GTTCGTCCTC GGATGGCCCT TGTACTTAGC CTTCAACGTT
       190        200        210        220        230        240
TCTGGCAGAC CCTACAATGG TTTCGCTTCC CATTTCTTCC CCAATGCTCC TATCTACAAC
       250        260        270        280        290        300
GACCGTGAAC GCCTCCAGAT TTACATCTCT GATGCTGGTA TTCTAGCCGT CTGTTATGGT
       310        320        330        340        350        360
CTTTACCGTT ACGCTGTTGC ACAAGGACTA GCCTCAATGA TCTGTCTAAA CGGAGTTCCG
       370        380        390        400        410        420
CTTCTGATAG TTAACTTTTT CCTCGTCTTG ATCACTTACT TACAACACAC TCACCCTGCG
       430        440        450        460        470        480
TTGCCTCACT ATGATTCATC AGAGTGGGAT TGGCTTAGAG GAGCTTTAGC TACTGTAGAC
       490        500        510        520        530        540
AGAGACTATG GAATCTTGAA CAAGGTGTTC CATAACATCA CAGACACCCA CGTCGCACAC
       550
CACT
```

FIG. 6

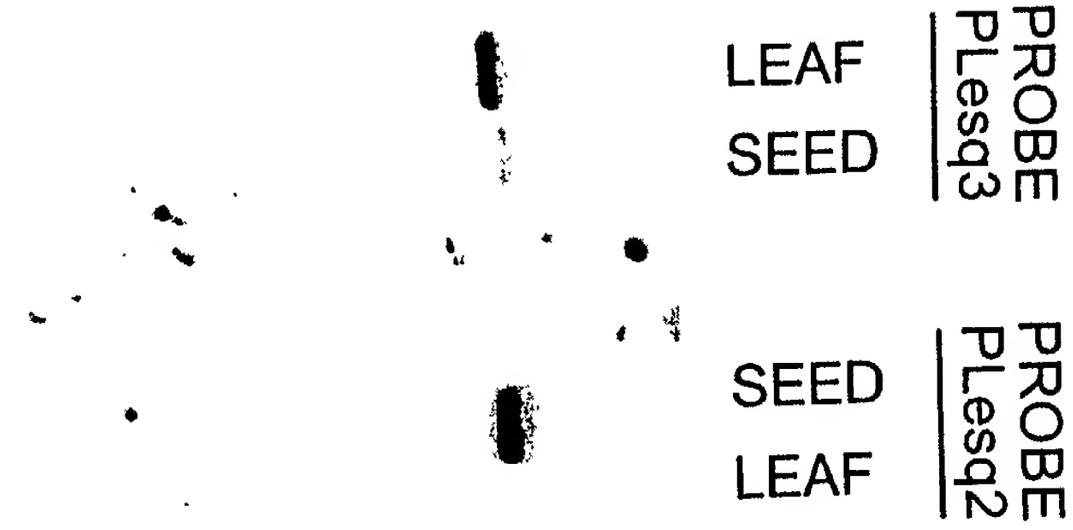


FIG. 7

```
 AT  GAA GCT TTA TAA GAA GTT AGT TTT CTC TGG TGA CAG AGA AAT TNT      47

GCT  AAT TGG TAG TGA CAG TTG AAG CAA CAG GAA CAA CAA GGA TGG TTG      95

GTG  NTG ATG CTG ATG TGG TGA TGT GTT ATT CAT CAA ATA CTA AAT ACT     143

ACA  TTA CTT GTT GCT GCC TAC TTC TCC TAT TTC CTC CGC CAC CCA TTT     191

TGG  ACC CAC GAN CCT TCC ATT TAA ACC CTC TCT CGT GCT ATT CAC CAG     239

AAG  AGA AGC CAA GAG AGA GAG AGA GAG AAT GTT CTG AGG ATC ATT GTC     287

TTC  TTC ATC GTT ATT AAC GTA AGT TTT TTT TGA CCA CTC ATA TCT AAA     335

ATC  TAG TAC ATG CAA TAG ATT AAT GAC TGT TCC TTC TTT TGA TAT TTT     383

                 Met Gly Ala Gly Gly Arg Ile Met Val Thr              10
CAG  CTT CTT GAA TTC AAG ATG GGT GCT GGT GGA AGA ATA ATG GTT ACC     431

Pro  Ser Ser Lys Lys Ser Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys      26
CCC  TCT TCC AAG AAA TCA GAA ACT GAA GCC CTA AAA CGT GGA CCA TGT     479

Glu  Lys Pro Pro Phe Thr Val Lys Asp Leu Lys Lys Ala ILe Pro Gln      42
GAG  AAA CCA CCA TTC ACT GTT AAA GAT CTG AAG AAA GCA ATC CCA CAG     527
```

FIG. 8A (CONT-1)

```
His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr     58
CAT TGT TTC AAG CGC TCT ATC CCT CGT TCT TTC TCC TAC CTT CTC ACA    575

Asp Ile Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe     74
GAT ATC ACT TTA GTT TCT TGC TTC TAC TAC GTT GCC ACA AAT TAC TTC    623

Ser Leu Leu Pro Gln Pro Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr     90
TCT CTT CTT CCT CAG CCT CTC TCT ACT TAC CTA GCT TGG CCT CTC TAT    671

Trp Val Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile Gly His    106
TGG GTA TGT CAA GGC TGT GTC TTA ACC GGT ATC TGG GTC ATT GGC CAT    719

Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr    122
GAA TGT GGT CAC CAT GCA TTC AGT GAC TAT CAA TGG GTA GAT GAC ACT    767

Val Gly Phe Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp    138
GTT GGT TTT ATC TTC CAT TCC TTC CTT CTC GTC CCT TAC TTC TCC TGG    815

Lys Tyr Ser His Arg Arg His His Ser Asn Asn Gly Ser Leu Glu Lys    154
AAA TAC AGT CAT CGT CGT CAC CAT TCC AAC AAT GGA TCT CTC GAG AAA    863

Asp Glu Val Phe Val Pro Pro Lys Lys Ala Ala Val Lys Trp Tyr Val    170
GAT GAA GTC TTT GTC CCA CCG AAG AAA GCT GCA GTC AAA TGG TAT GTT    911

Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Leu Val Leu Thr Val Gln    186
AAA TAC CTC AAC AAC CCT CTT GGA CGC ATT CTG GTG TTA ACA GTT CAG    959
```

FIG. 8A (CONT-2)

Phe Ile Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg 202
TTT ATC CTC GGG TGG CCT TTG TAT CTA GCC TTT AAT GTA TCA GGT AGA 1007

Pro Tyr Asp Gly Phe Ala Ser His Phe Phe Pro His Ala Pro Ile Phe 218
CCT TAT GAT GGT TTC GCT TCA CAT TTC TTC CCT CAT GCA CCT ATC TTT 1055

Lys Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu 234
AAA GAC CGA GAA CGC CTC CAG ATA TAC ATC TCA GAT GCT GGT ATT CTA 1103

Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr 250
GCT GTC TGT TAT GGT CTT TAC CGT TAC GCT GCT TCA CAA GGA TTG ACT 1151

Ala Met Ile Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Phe Phe 266
GCT ATG ATC TGC GTC TAT GGA GTA CCG CTT TTG ATA GTG AAC TTT TTC 1199

Leu Val Leu Val Thr Phe Leu Gln His Thr His Pro Ser Leu Pro His 282
CTT GTC TTG GTA ACT TTC TTG CAG CAC ACT CAT CCT TCG TTA CCT CAT 1247

Tyr Asp Ser Thr Glu Trp Glu Trp Ile Arg Gly Ala Leu Val Thr Val 298
TAT GAT TCA ACC GAG TGG GAA TGG ATT AGA GGA GCT TTG GTT ACG GTA 1295

Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp 314
GAC AGA GAC TAT GGA ATA TTG AAC AAG GTG TTC CAT AAC ATA ACA GAC 1343

Thr His Val Ala His His Leu Phe Ala Thr Ile Pro His Tyr Asn Ala 330
ACA CAT GTG GCT CAT CAT CTC TTT GCA ACT ATA CCG CAT TAT AAC GCA 1391

FIG. 8B (CONT-1)

```
Met Glu Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His      346
ATG GAA GCT ACA GAG GCG ATA AAG CCA ATA CTT GGT GAT TAC TAC CAC     1439

Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu      362
TTC GAT GGA ACA CCG TGG TAT GTG GCC ATG TAT AGG GAA GCA AAG GAG     1487

Cys Leu Tyr Val Glu Pro Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr      378
TGT CTC TAT GTA GAA CCG GAT ACG GAA CGT GGG AAG AAA GGT GTC TAC     1535

Tyr Tyr Asn Asn Lys Leu                                              384
TAT TAC AAC AAT AAG TTA TGA GGC TGA TAG GGC GAG AGA AGT GCA ATT     1583

ATC AAT CTT CAT TTC CAT GTT TTA GGT GTC TTG TTT AAG AAG CTA TGC     1631

TTT GTT TCA ATA ATC TCA GAG TCC ATN TAG TTG TGT TCT GGT GCA TTT     1679

TGC CTA GTT ATG TGG TGT CGG AAG TTA GTG TTC AAA CTG CTT CCT GCT     1727

GTG CTG CCC AGT GAA GAA CAA GTT TAC GTG TTT AAA ATA CTC GGA ACG     1775

AAT TGA CCA CAA NAT ATC CAA AAC CGG CTA TCC GAA TTC CAT ATC CGA     1823

AAA CCG GAT ATC CAA ATT TCC AGA GTA CTT AG                          1855
```

FIG. 8B (CONT-2)

		10	20	30	40	50	
LFFAH12	1	MGAGGRIM--	--VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	50
FAH12	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	DLKRAIPPHC	50
ATFAD2	1	MGAGGRMP--	--VPTSSKKS	--ETDTTKRV	PCEKPPFSVG	DLKKAIPPHC	50
BNFAD2	1	MGAGGRMQ--	--VSPPSKKS	--ETDNIKRV	PCETPPFTVG	ELKKAIPPHC	50
GMFAD2-1	1	MGLA-KETTM	GGRGRVAKVE	VQGKKPLSRV	PNTKPPFTVG	QLKKAIPPHC	50
GMFAD2-2	1	MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPQFSLS	QIKKAIPPHC	50
ZMFAD2	1	MGAGGRMTEK	EREKQEQLAR	ATGGAAMQRS	PVEKPPFTLG	QIKKAIPPHC	50
RCFAD2	1	----------	----------	----------	----------	----------	50

		60	70	80	90	100	
LFFAH12	51	FKRSIPRSFS	YLLTDITLVS	CFYYVATNYF	SLLPQPLSTY	LAWPLYWVCQ	100
FAH12	51	FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	VAWLVYWLFQ	100
ATFAD2	51	FKRSIPRSFS	YLISDIIIAS	CFYYVATNYF	SLLPQPLS-Y	LAWPLYWACQ	100
BNFAD2	51	FKRSIPRSFS	HLIWDIIIAS	CFYYVATTYF	PLLPNPLS-Y	FAWPLYWACQ	100
GMFAD2-1	51	FQRSLLTSFS	YVVYDLSFAF	IFY-IATTYF	HLLPQPFS-L	IAWPIYWVLQ	100
GMFAD2-2	51	FQRSVLRSFS	YVVYDLTIAF	CLYYVATHYF	HLLPGPLS-F	RGMAIYWAVQ	100
ZMFAD2	51	FERSVLKSFS	YVVHDLVIAA	ALLYFALAII	PALPSPLR-Y	AAWPLYWIAQ	100
RCFAD2	1	----------	----------	----------	----------	----------	100

		110	120	130	140	150	
LFFAH12	101	GCVLTGIWVI	GHECGHHAFS	DYQWVDDTVG	FIFHSFLLVP	YFSWKYSHRR	150
FAH12	101	GCILTGLWVI	GHECGHHAFS	EYQLADDIVG	LIVHSALLVP	YFSWKYSHRR	150
ATFAD2	101	GCVLTGIWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
BNFAD2	101	GCVLTGVWVI	AHECGHAAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
GMFAD2-1	101	GCLLTGVWVI	AHECGHHAFS	KYQWVDDVVG	LTLHSTLLVP	YFSWKISHRR	150
GMFAD2-2	101	GCILTGVWVI	AHECGHHAFS	DYQLLDDIVG	LILHSALLVP	YFSWKYSHRR	150
ZMFAD2	101	G---------	-------AFS	DYSLLDDVVG	LVLHSSLMVP	YFSWKYSHRR	150
RCFAD2	101	-------WVM	AHDCGHHAFS	DYQLLDDVVG	LILHSCLLVP	YFSWKHSHRR	150

FIG. 9A (CONT-1)

		160	170	180	190	200	
LFFAH12	151	HHSNNGSLEK	DEVFVPPKKA	AVKWYVKYL-	NNPLGRILVL	TVQFILGWPL	200
FAH12	151	HHSNIGSLER	DEVFVPKSKS	KISWYSKYS-	NNPPGRVLTL	AATLLLGWPL	200
ATFAD2	151	HHSNTGSLER	DEVFVPKQKS	AIKWYGKYL-	NNPLGRIMML	TVQFVLGWPL	200
BNFAD2	151	HHSNTGSLER	DEVFVPR-RS	QTSSGTAST-	STTFGRTVML	TVQFTLGWPL	200
GMFAD2-1	151	HHSNTGSLDR	DEVFVPKPKS	KVAWFSKYL-	NNPLGRAVSL	LVTLTIGWPM	200
GMFAD2-2	151	HHSNTGSLER	DEVFVPKQKS	CIKWYSKYL-	NNPPGRVLTL	AVTLTLGWPL	200
ZMFAD2	151	HHSNTGSLER	DEVFVPKKKE	ALPWYTPYVY	NNPVGRVVHI	VVQLTLGWPL	200
RCFAD2	151	HHSNTGSLER	DEVFVPKKKS	SIRWYSKYL-	NNPPGRIMTI	AVTLSLGWPL	200
		210	220	230	240	250	
LFFAH12	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR	250
FAH12	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFVLYQ	250
ATFAD2	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYLSDAG	ILAVCFGLYR	250
BNFAD2	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	ILAVCYGLLP	250
GMFAD2-1	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSDVA	LFSVTYSLYR	250
GMFAD2-2	201	YLALNVSGRP	YDR-FACHYD	PYGPIYSDRE	RLQIYISDAG	VLAVVYGLFR	250
ZMFAD2	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK	250
RCFAD2	201	YLAFNVSGRP	YPR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLAVTFGLYQ	250

FIG. 9A (CONT-2)

```
                    260         270         280         290         300
LFFAH12    251  YAASQGLTAM  ICVYGVPLLI  VNFFLVLVTF  LQHTHPSLPH  YDSTEWEWIR    300
FAH12      251  ATMAKGLAWV  MRIYGVPLLI  VNCFLVMITY  LQHTHPAIPR  YGSSEWDWLR    300
ATFAD2     251  YAAAQGMASM  ICLYGVPLLI  VNAFLVLITY  LQHTHPSLPH  YDSSEWDWLR    300
BNFAD2     251  YAAVQGVASM  VCFLRVPLLI  VNGFLVLITY  LQHTHPSLPH  YDSSEWDWLR    300
GMFAD2-1   251  VATLKGLVWL  LCVYGVPLLI  VNGFLVTITY  LQHTHFALPH  YDSSEWDWLK    300
GMFAD2-2   251  LAMAKGLAWV  VCVYGVPLLV  VNGFLVLITF  LQHTHPALPH  YTSSEWDWLR    300
ZMFAD2     251  LAAAFGVWWV  VRVYAVPLLI  VNAWLVLITY  LQHTHPSLPH  YDSSEWDWLR    300
RCFAD2     251  LAIAKGLAWV  VCVYGVPLLV  VNSFLVLITF  LQHTHPALPH  YDSSEWDWLR    300

                    310         320         330         340         350
LFFAH12    301  GALVTVDRDY  GILNKVFHNI  TDTHVAHHLF  ATIPHYNAME  ATEAIKPILG    350
FAH12      301  GAMVTVDRDY  GVLNKVFHNI  ADTHVAHHLF  ATVPHYHAME  ATKAIKPIMG    350
ATFAD2     301  GALATVDRDY  GILNKVFHNI  TDTHVAHHLF  STMPHYNAME  ATKAIKPILG    350
BNFAD2     301  GALATVDRDY  GILNQGFHNI  TDTHEAHHLF  STMPHYHAME  ATKAIKPILG    350
GMFAD2-1   301  GALATMDRDY  GILNKVFHHI  TDTHVAHHLF  STMPHYHAME  ATNAIKPILG    350
GMFAD2-2   301  GALATVDRDY  GILNKVFHNI  TDTHVAHHLF  STMPHYHAME  ATKAIKPILG    350
ZMFAD2     301  GALATMDRDY  GILNRVFHNI  TDTHVAHHLF  STMPHYHAME  ATKAIRPILG    350
RCFAD2     301  GALATVDRDY  GILNKVFHNI  TDTQVAHHLF  ----------  ----------    350

                    360         370         380         390         400
LFFAH12    351  DYYHFDGTPW  YVAMYREAKE  CLYVEPDTER  GKKGVYYYNN  K-L.......    400
FAH12      351  EYYRYDGTPF  YKALWREAKE  CLFVEPDEGA  PTQGVFWYRN  KY-.......    400
ATFAD2     351  DYYQFDGTPW  YVAMYREAKE  CIYVEPDREG  DKKGVYWYNN  K-L.......    400
BNFAD2     351  EYYQFDGTPV  YKAMWREAKE  CIYVEPDRQG  EKKGVFWYNN  KL*.......    400
GMFAD2-1   351  EYYQFDDTPF  YKALWREARE  CLYVEPDEGT  SEKGVYWYRN  KY*.......    400
GMFAD2-2   351  EYYRFDETPF  VKAMWREARE  CIYVEPDQST  ESKGVFWYNN  KL-.......    400
ZMFAD2     351  DYYHFDPTPV  AKATWREAGE  CIYVEPE---  DRKGVFWYNK  KF*.......    400
```

FIG. 9B

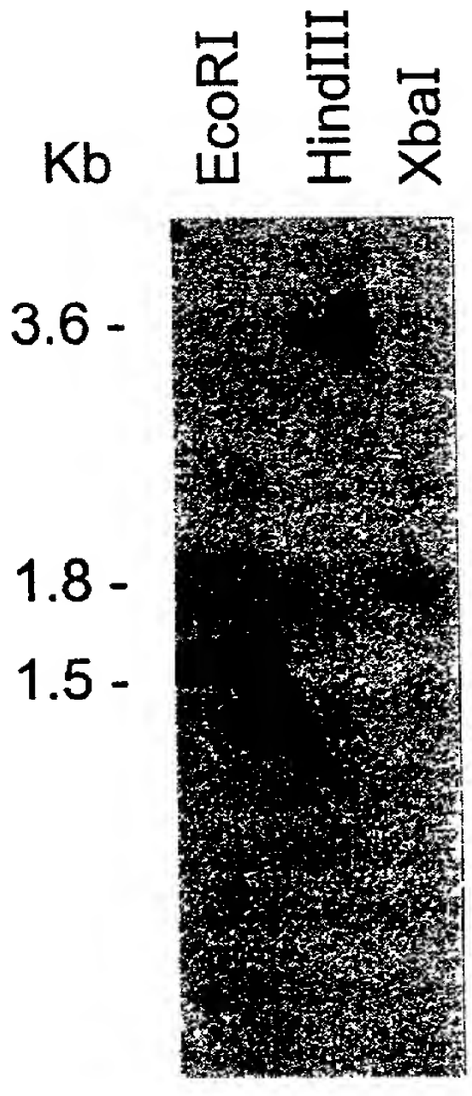


FIG. 10

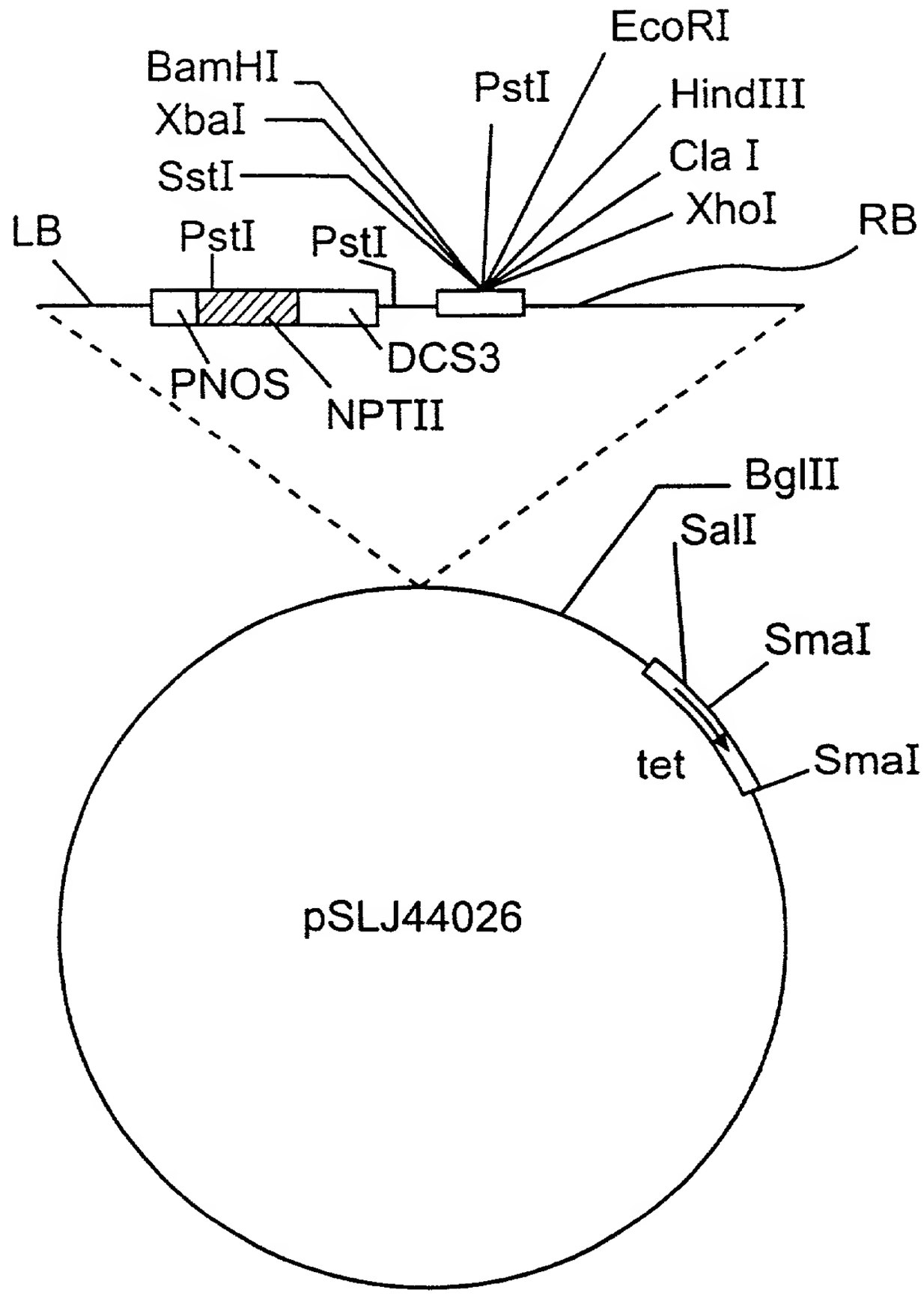

EcoRI
BamHI
PstI
HindIII
XbaI
Cla I
SstI
XhoI
RB
LB
PstI
PstI
DCS3
PNOS
NPTII
BglII
SalI
SmaI
tet
SmaI
pSLJ44026

FIG. 11